RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/567,074

Source: TFWP

Date Processed by STIC: 02/21/2006

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/567,074_   CRF Edit Date: _02/21/2006_
                                  Edited by: _DA_

_____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

_____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

_____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

_✓_ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

_____ Inserted mandatory headings/numeric identifiers, specifically:

_____

_____ Moved responses to same line as heading/numeric identifier, specifically:

_____

_____ Other:

_____
_____
_____

IFWP

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     5 <110> APPLICANT: Scherer, Stephen W.
     7         Minassian, Berge A.
    11 <120> TITLE OF INVENTION: Lafora's Disease Gene
    15 <130> FILE REFERENCE: 4012.1000-003
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/567,074
C--> 19 <141> CURRENT FILING DATE: 2006-02-03
    19 <150> PRIOR APPLICATION NUMBER: PCT/CA2004/001449
    21 <151> PRIOR FILING DATE: 2004-07-30
    25 <150> PRIOR APPLICATION NUMBER: US 60/491,968
    27 <151> PRIOR FILING DATE: 2003-08-04
    31 <160> NUMBER OF SEQ ID NOS: 5
    35 <170> SOFTWARE: PatentIn version 3.1
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    41 <211> LENGTH: 2120
    43 <212> TYPE: DNA
    45 <213> ORGANISM: Homo sapiens
    49 <400> SEQUENCE: 1
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    52 atcagcctgc tcgagtgcaa ggtgtgcttt gagaagtttg gccaccggca gcagcggcgc    120
    54 ccgcgcaacc tgtcctgcgg ccacgtggtc tgcctggcct gcgtggccgc cctggcgcac    180
    56 ccgcgcactc tggccctcga gtgcccattc tgcaggcgag cttgccgggg ctgcgacacc    240
    58 agcgactgcc tgccggtgct gcacctcata gagctcctgg gctcagcgct tcgccagtcc    300
    60 ccggccgccc atcgcgccgc ccccagcgcc cccggagccc tcacctgcca ccacaccttc    360
    62 ggcggctggg ggaccctggt caaccccacc ggactggcgc tttgtcccaa gacggggcgt    420
    64 gtcgtggtgg tgcacgacgg caggaggcgt gtcaagattt ttgactcagg gggaggatgc    480
    66 gcgcatcagt ttggagagaa gggggacgct gcccaagaca ttaggtaccc tgtggatgtc    540
    68 accatcacca acgactgcca tgtggttgtc actgacgccg gcgatcgctc catcaaagtg    600
    70 tttgattttt ttggccagat caagcttgtc attggaggcc aattctcctt accttggggt    660
    72 gtggagacca cccctcagaa tgggattgtg gtaactgatg cggaggcagg gtccctgcac    720
    74 ctcctggacg tcgacttcgc ggaaggggtc cttcggagaa ctgaaaggtt gcaagctcat    780
    76 ctgtgcaatc cccgaggggt ggcagtgtct tggctcaccg gggccattgc ggtcctggag    840
    78 cacccctgg ccctggggac tggggtttgc agcaccaggg tgaaagtgtt tagctcaagt     900
    80 atgcagcttg tcggccaagt ggatacctt gggctgagcc tctactttcc ctccaaaata     960
    82 actgcctccg ctgtgacctt tgatcaccag ggaaatgtga ttgttgcaga tacatctggt    1020
    84 ccagctatcc tttgcttagg aaaacctgag gagtttccag taccgaagcc catggtcact    1080
    86 catggtcttt cgcatcctgt ggctcttacc ttcaccaagg agaattctct tcttgtgctg    1140
    88 gacacagcat ctcattctat aaaagtctat aaagttgact gggggtgatg ggctggggtg    1200
    90 ggtccctgga atcagaagca ctagtgctgc cattaatgaa ttgtttaacc ctggataagt    1260
    92 cacttaaact catctatcca ggcagggata attaaaacca tctggcagac ttacaaagct    1320
    94 tgggacagtt attggagatt aatctaccat ttattgaatg catactctgt gcaaggaaat    1380
    96 ttgcaaatat tagcttattt aatctgtact atccagtgag gtaatttctt ccccccccag    1440
    98 atagagtcaa gctctgtcac ccaggctgga gtgcagaagc atgatcacag ctcactacag    1500
   100 tttcaacgtc ccccgctcag gtggtccttc cacctcagcc tcccaagtag ctgggaccac    1560
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RAW SEQUENCE LISTING   DATE: 02/21/2006
PATENT APPLICATION: US/10/567,074   TIME: 15:23:49

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\02212006\J567074.raw

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106 agtactagga gtacaggcat agccacttgc tcagccataa tttttattat taatctcatt   1740
108 gtacaagtga gaaaactgag acccagagag cttaagtgac ttcctcgagg tcatagttac   1800
110 ttactgcctt agtcccaatt tgaattcaat tctgattcca aataagttgc gcttaaataa   1860
112 gacaacagat gtgggaaaaa tatgtgaatg tgtagtgttg ctatgtgtac tgtctttaca   1920
114 agtagctaat tattttagca caaagatgtg caaagaaagg agactttatg gagagttcag   1980
116 gagaaaaagg attttgtggt ggccatcact ttcattcaat ttgcgactgc tctgatggca   2040
118 cattagatga agttactgtt gatcctgagt tacgtgaata agaaaaacaa ttgaactgct   2100
120 tattaaaaaa gtaaacatgt                                                2120
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125 <211> LENGTH: 395
127 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
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140          20                  25                  30
143 Phe Gly His Arg Gln Gln Arg Arg Pro Arg Asn Leu Ser Cys Gly His
144          35                  40                  45
147 Val Val Cys Leu Ala Cys Val Ala Ala Leu Ala His Pro Arg Thr Leu
148      50                  55                  60
151 Ala Leu Glu Cys Pro Phe Cys Arg Arg Ala Cys Arg Gly Cys Asp Thr
152 65                  70                  75                  80
155 Ser Asp Cys Leu Pro Val Leu His Leu Ile Glu Leu Leu Gly Ser Ala
156              85                  90                  95
159 Leu Arg Gln Ser Pro Ala Ala His Arg Ala Ala Pro Ser Ala Pro Gly
160              100                 105                 110
163 Ala Leu Thr Cys His His Thr Phe Gly Gly Trp Gly Thr Leu Val Asn
164              115                 120                 125
167 Pro Thr Gly Leu Ala Leu Cys Pro Lys Thr Gly Arg Val Val Val Val
168      130                 135                 140
171 His Asp Gly Arg Arg Arg Val Lys Ile Phe Asp Ser Gly Gly Gly Cys
172 145                 150                 155                 160
175 Ala His Gln Phe Gly Glu Lys Gly Asp Ala Ala Gln Asp Ile Arg Tyr
176              165                 170                 175
179 Pro Val Asp Val Thr Ile Thr Asn Asp Cys His Val Val Val Thr Asp
180              180                 185                 190
183 Ala Gly Asp Arg Ser Ile Lys Val Phe Asp Phe Phe Gly Gln Ile Lys
184              195                 200                 205
187 Leu Val Ile Gly Gly Gln Phe Ser Leu Pro Trp Gly Val Glu Thr Thr
188      210                 215                 220
191 Pro Gln Asn Gly Ile Val Val Thr Asp Ala Glu Ala Gly Ser Leu His
192 225                 230                 235                 240
195 Leu Leu Asp Val Asp Phe Ala Glu Gly Val Leu Arg Arg Thr Glu Arg
196              245                 250                 255
199 Leu Gln Ala His Leu Cys Asn Pro Arg Gly Val Ala Val Ser Trp Leu
200              260                 265                 270
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203 Thr Gly Ala Ile Ala Val Leu Glu His Pro Leu Ala Leu Gly Thr Gly
204         275                 280                 285
207 Val Cys Ser Thr Arg Val Lys Val Phe Ser Ser Ser Met Gln Leu Val
208         290                 295                 300
211 Gly Gln Val Asp Thr Phe Gly Leu Ser Leu Tyr Phe Pro Ser Lys Ile
212 305                 310                 315                 320
215 Thr Ala Ser Ala Val Thr Phe Asp His Gln Gly Asn Val Ile Val Ala
216                 325                 330                 335
219 Asp Thr Ser Gly Pro Ala Ile Leu Cys Leu Gly Lys Pro Glu Glu Phe
220                 340                 345                 350
223 Pro Val Pro Lys Pro Met Val Thr His Gly Leu Ser His Pro Val Ala
224         355                 360                 365
227 Leu Thr Phe Thr Lys Glu Asn Ser Leu Leu Val Leu Asp Thr Ala Ser
228         370                 375                 380
231 His Ser Ile Lys Val Tyr Lys Val Asp Trp Gly
232 385                 390                 395
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237 <211> LENGTH: 3008
239 <212> TYPE· DNA
241 <213> ORGANISM: Canis sp.
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247 <221> NAME/KEY: CDS
249 <222> LOCATION: (698)..(1897)
251 <223> OTHER INFORMATION:
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257 <221> NAME/KEY: misc_feature
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261 <223> OTHER INFORMATION: N=any nucleic acid
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279 <222> LOCATION: (2750)..(2750)
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311 <223> OTHER INFORMATION: N=any nucleic acid
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351 <223> OTHER INFORMATION: N=any nucleic acid
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358 gccccaagcc ccccaggttc ccggccccaa gaaccaagcc ccccggcccc ccgcccccag     120
360 cacccagcac caagcccccg ccccccgccc caagcaccca gccccagcac ccagcccccg     180
362 ccccagcccc agccccagca cccagccccc gccccagcac ccagccccag cacccagccc     240
364 ccgccccagc cccagccccc gtccccccccc ccagcaccca gccccagccc cagcagcagc    300
366 acccagcagg ggactgcaaa gcgtaggcta ccccaggtgg aacaccgtgt tctagttttg     360
368 ctttgccgtt tgcagcctgg gcgatcgggg gccaccgctc gagcctgttt cccgtcgcgg     420
370 aaagcggagc cgccccgccc cgccccccgc ctgcctgaag gtcacgggcc tgggcctgcg     480
372 gcgcgcggtg cggcccgcga gcgtccgctc ccgcgccctc cgcagtcagc gcccgcccgc     540
374 ccgccggggg accgcaggcc gcggccgaga ggctgcgcgc tgcgcccgcg acgtcaggcc     600
376 ccgccccgcc ccgccccgcc ccgtgaccgg ccccggcccc ggccccggcc ccggcccccgg    660
378 accgagcggc gcccgcggga gcggcggcgg ccgcgcg atg ggg gcc gaa gcg gcg      715
379                                            Met Gly Ala Glu Ala Ala
380                                            1               5
382 ggg agc ggg cgg gcg ctg cgg gag ctg gtg cgc gag gcc gag gtc agc      763
383 Gly Ser Gly Arg Ala Leu Arg Glu Leu Val Arg Glu Ala Glu Val Ser
384         10              15                  20
386 ttg ctc gag tgc aag gtg tgc ttc gag agg ttc ggc cac cgc cag cag      811
387 Leu Leu Glu Cys Lys Val Cys Phe Glu Arg Phe Gly His Arg Gln Gln
388         25              30                  35
390 cgg cgc ccg cgc aac ctg ccc tgc ggc cac gtg gtg tgc ctg gcc tgc      859
391 Arg Arg Pro Arg Asn Leu Pro Cys Gly His Val Val Cys Leu Ala Cys
392     40              45                  50
394 gtg gcg gcc ctg gcg cac ccg cgg acg ctg gcc ctg gag tgc ccc ttc      907
395 Val Ala Ala Leu Ala His Pro Arg Thr Leu Ala Leu Glu Cys Pro Phe
396 55              60                  65                  70
398 tgc cgc cgg gcc tgc cgc ggc tgc gac acc agc gac tgc ctg ccg gtg      955
399 Cys Arg Arg Ala Cys Arg Gly Cys Asp Thr Ser Asp Cys Leu Pro Val
400             75                  80                  85
402 ctt cac ctc ctg gag ctc ctg ggc tcg gcg ctg cgc cca gcc ccc gcc     1003
403 Leu His Leu Leu Glu Leu Leu Gly Ser Ala Leu Arg Pro Ala Pro Ala
404         90                  95                  100
406 gcc ccc cgc gcc gcc ccc cgc gcc gcc ccc tgc gcc ccg ggc gcc ctc     1051
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407 Ala Pro Arg Ala Ala Pro Arg Ala Ala Pro Cys Ala Pro Gly Ala Leu
408         105             110             115
410 gcc tgc cat cac gcg ttc gga ggc tgg ggg acc ctg gtc aac ccc acg      1099
411 Ala Cys His His Ala Phe Gly Gly Trp Gly Thr Leu Val Asn Pro Thr
412     120             125             130
414 ggg ctg gcg ctg tgc ccc aag acc ggg cgg gtc gtg gtg gtg cac gac      1147
415 Gly Leu Ala Leu Cys Pro Lys Thr Gly Arg Val Val Val Val His Asp
416 135             140             145             150
418 ggc agg agg cgg gtc aag atc ttt gac tcc ggg gga gga tgc gcc cat      1195
419 Gly Arg Arg Arg Val Lys Ile Phe Asp Ser Gly Gly Gly Cys Ala His
420             155             160             165
422 cag ttt gga gag aag ggg gag gct gcc cag gac att agg tac ccc ctg      1243
423 Gln Phe Gly Glu Lys Gly Glu Ala Ala Gln Asp Ile Arg Tyr Pro Leu
424             170             175             180
426 gac gtc gcc gtc acc aac gac tgc cac gtg gtt gtc acc gac gcc ggc      1291
427 Asp Val Ala Val Thr Asn Asp Cys His Val Val Val Thr Asp Ala Gly
428         185             190             195
430 gac cgc tcc atc aaa gtg ttt gat ttc ttt ggc cag atc aag ctc gtc      1339
431 Asp Arg Ser Ile Lys Val Phe Asp Phe Phe Gly Gln Ile Lys Leu Val
432     200             205             210
434 att gga gac cag ttt tcc tta cct tgg ggc gtg gag acc acc cct cag      1387
435 Ile Gly Asp Gln Phe Ser Leu Pro Trp Gly Val Glu Thr Thr Pro Gln
436 215             220             225             230
438 aat ggg gtc gtg gta act gac gcc gag gca ggg tcg ctg cac ctg ctg      1435
439 Asn Gly Val Val Val Thr Asp Ala Glu Ala Gly Ser Leu His Leu Leu
440             235             240             245
442 gaa gtc gac ttt gca gaa gga gcc ctc cag agg act gaa aag ctg caa      1483
443 Glu Val Asp Phe Ala Glu Gly Ala Leu Gln Arg Thr Glu Lys Leu Gln
444             250             255             260
446 ggt cat ctg tgc aac ccg cga ggg gtg gcc gtg tcc tgg ctc act ggg      1531
447 Gly His Leu Cys Asn Pro Arg Gly Val Ala Val Ser Trp Leu Thr Gly
448         265             270             275
450 gcc att gcg gtc ctg gag cac cct ccg ggg ctg ggg gct ggg gcg ggc      1579
451 Ala Ile Ala Val Leu Glu His Pro Pro Gly Leu Gly Ala Gly Ala Gly
452     280             285             290
454 agc acc gcc gtg aag gtg ttc agc cca act atg cag ctg atc ggc cag      1627
455 Ser Thr Ala Val Lys Val Phe Ser Pro Thr Met Gln Leu Ile Gly Gln
456 295             300             305             310
458 gtg gat acc ttt ggg ctc agc ctc ttt ttc ccc tct aga ata acc gcc      1675
459 Val Asp Thr Phe Gly Leu Ser Leu Phe Phe Pro Ser Arg Ile Thr Ala
460             315             320             325
462 tcc gcc gtg acc ttt gat cac cag ggg aat gtg att gtt gca gat act      1723
463 Ser Ala Val Thr Phe Asp His Gln Gly Asn Val Ile Val Ala Asp Thr
464             330             335             340
466 tct agt cag gcc gtc cta tgc ttg gga cag cct gag gaa ttt cca gtc      1771
467 Ser Ser Gln Ala Val Leu Cys Leu Gly Gln Pro Glu Glu Phe Pro Val
468         345             350             355
470 ctg aag ccc atc atc acc cat ggt ctt tcc cat cct gtg gca ctg acc      1819
471 Leu Lys Pro Ile Ile Thr His Gly Leu Ser His Pro Val Ala Leu Thr
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/21/2006
PATENT APPLICATION: US/10/567,074   TIME: 15:23:50

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\02212006\J567074.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 2692,2748,2750,2793,2845,2916,2918,2931,2941,2990

VERIFICATION SUMMARY   DATE: 02/21/2006
PATENT APPLICATION: **US/10/567,074**   TIME: 15:23:50

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\02212006\J567074.raw**

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L:19  M:270 C: Current Application Number differs, Replaced Current Application No
L:19  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:265 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:251
L:506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2637
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2697
L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2757
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2817
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2877
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2937
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**Raw Sequence Listing before editing,
for reference only**

IFWP

RAW SEQUENCE LISTING   DATE: 02/10/2006
PATENT APPLICATION: US/10/567,074   TIME: 08:37:03

Input Set : **A:\40121000003.txt**
Output Set: **N:\CRF4\02102006\J567074.raw**

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     5 <110> APPLICANT: Scherer, Stephen W.
     7        Minassian, Berge A.
    11 <120> TITLE OF INVENTION: Lafora's Disease Gene
    15 <130> FILE REFERENCE: 4012.1000-003
C--> 19 <140> CURRENT APPLICATION NUMBER: US/10/567,074
C--> 19 <141> CURRENT FILING DATE: 2006-02-03
    19 <150> PRIOR APPLICATION NUMBER: PCT/CA2004/001449
    21 <151> PRIOR FILING DATE: 2004-07-30
    25 <150> PRIOR APPLICATION NUMBER: US 60/491,968
    27 <151> PRIOR FILING DATE: 2003-08-04
    31 <160> NUMBER OF SEQ ID NOS: 5
    35 <170> SOFTWARE: PatentIn version 3.1
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Does Not Comply
Corrected Diskette Needed
(p9-1)

ERRORED SEQUENCES

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   714 <210> SEQ ID NO: 5
   716 <211> LENGTH: 12
   718 <212> TYPE: DNA
   720 <213> ORGANISM: Canis sp.
   724 <400> SEQUENCE: 5
   725 gccgcccccc gc                                        12
E--> 729 4012.1000-003
E--> 730 1/13              -> deleted
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VERIFICATION SUMMARY   DATE: 02/10/2006
PATENT APPLICATION: **US/10/567,074**   TIME: 08:37:04

Input Set : **A:\40121000003.txt**
Output Set: **N:\CRF4\02102006\J567074.raw**

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L:19  M:270 C: Current Application Number differs, Replaced Current Application No
L:19  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:265 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:251
L:506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2637
L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2697
L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2757
L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2817
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2877
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2937
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L:729 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:730 M:254 E: No. of Bases conflict, LENGTH:Input:13 Counted:15 SEQ:5
L:730 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:730 M:252 E: No. of Seq. differs, <211> LENGTH:Input:12 Found:15 SEQ:5
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